

1644

四庫全書

APK 1 1/1

TECH CENTER 1600, 2300

DATE: 03/30/2001  
TIME: 15:44:51

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/707,468A

Input Set : A:\Mor00031.app  
Output Set: N:\CRF3\03302001\I707468A.raw

3 <110> APPLICANT: Nicolaides, Nicholas C  
4 Grasso, Luigi  
5 Sass, Philip M  
7 <120> TITLE OF INVENTION: METHODS FOR GENERATING GENETICALLY ALTERED  
8 ANTIBODY-PRODUCING CELL LINES WITH IMPROVED ANTIBODY  
9 CHARACTERISTICS  
11 <130> FILE REFERENCE: MOR-0003  
13 <140> CURRENT APPLICATION NUMBER: 09/707,468A  
14 <141> CURRENT FILING DATE: 2000-11-07  
16 <160> NUMBER OF SEQ ID NOS: 16  
18 <170> SOFTWARE: PatentIn Ver. 2.1  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 24  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Artificial Sequence  
25 <220> FEATURE:  
26 <223> OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide  
27 primer  
29 <400> SEQUENCE: 1 24  
30 ggattttcag gtgcagattt tcag  
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34 <211> LENGTH: 21  
35 <212> TYPE: DNA  
36 <213> ORGANISM: Artificial Sequence  
38 <220> FEATURE:  
39 <223> OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide  
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46 <210> SEQ ID NO: 3  
47 <211> LENGTH: 19  
48 <212> TYPE: DNA  
49 <213> ORGANISM: Artificial Sequence  
51 <220> FEATURE:  
52 <223> OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide  
53 primer  
55 <220> FEATURE:  
56 <221> NAME/KEY: misc\_feature  
57 <222> LOCATION: (5)  
58 <223> OTHER INFORMATION: A or G or C or T/U  
60 <220> FEATURE:  
61 <221> NAME/KEY: misc\_feature  
62 <222> LOCATION: (11)  
63 <223> OTHER INFORMATION: A or G or C or T/U  
65 <400> SEQUENCE: 3  
66 akgtnmagct ncagsagt  
69 <210> SEQ ID NO: 4 19

**ENTERED**

24

21

19

3/30/01

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70 <211> LENGTH: 19  
71 <212> TYPE: DNA  
72 <213> ORGANISM: Artificial Sequence  
74 <220> FEATURE: Description of Artificial Sequence: oligonucleotide  
75 <223> OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide  
76 primer  
78 <220> FEATURE:  
79 <221> NAME/KEY: misc\_feature  
80 <222> LOCATION: (2)  
81 <223> OTHER INFORMATION: A or G or C or T/U  
83 <400> SEQUENCE: 4 19  
  
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88 <211> LENGTH: 859  
89 <212> TYPE: PRT  
90 <213> ORGANISM: Mus musculus  
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94 1 5 10  
95 Pro Ile Asp Gly Lys Ser Val His Gln Ile Cys Ser Gly Gln Val Ile 30  
96 20 25  
97 Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Ile Glu Asn Ser Val Asp 45  
99 35 40  
100 Ala Gly Ala Thr Thr Ile Asp Leu Arg Leu Lys Asp Tyr Gly Val Asp 60  
101 50 55  
102 Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Asn Phe 80  
103 65 70 75  
104 Glu Gly Leu Ala Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala 95  
105 85 90  
106 Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser 110  
107 100 105  
108 Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Gly Ser 125  
109 115 120  
110 Ala Ser Val Gly Thr Arg Leu Val Phe Asp His Asn Gly Lys Ile Thr 140  
111 130 135  
112 Gln Lys Thr Pro Tyr Pro Arg Pro Lys Gly Thr Thr Val Ser Val Gln 160  
113 145 150 155  
114 His Leu Phe Tyr Thr Leu Pro Val Arg Tyr Lys Glu Phe Gln Arg Asn 175  
115 165 170  
116 Ile Lys Lys Glu Tyr Ser Lys Met Val Gln Val Leu Gln Ala Tyr Cys 190  
117 180 185  
118 Ile Ile Ser Ala Gly Val Arg Val Ser Cys Thr Asn Gln Leu Gly Gln 205  
119 195 200  
120 Gly Lys Arg His Ala Val Val Cys Thr Ser Gly Thr Ser Gly Met Lys 220  
121 210 215  
122 Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile 240  
123 225 230 235  
124 Pro Phe Val Gln Leu Pro Pro Ser Asp Ala Val Cys Glu Glu Tyr Gly 255  
125 245  
126 250  
127 255

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141 Leu Ser Thr Ser Gly Arg His Lys Thr Phe Ser Thr Phe Arg Ala Ser  
142 260 265 270  
144 Phe His Ser Ala Arg Thr Ala Pro Gly Gly Val Gln Gln Thr Gly Ser  
145 275 280 285  
147 Phe Ser Ser Ser Ile Arg Gly Pro Val Thr Gln Gln Arg Ser Leu Ser  
148 290 295 300  
150 Leu Ser Met Arg Phe Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe  
151 305 310 315 320  
153 Val Val Leu Asn Val Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val  
154 325 330 335  
156 Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu  
157 340 345 350  
159 Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Ala Asn  
160 355 360 365  
162 Lys Leu Asn Val Asn Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu  
163 370 375 380  
165 Val Lys Leu His Thr Ala Glu Leu Glu Lys Pro Val Pro Gly Lys Gln  
166 385 390 395 400  
168 Asp Asn Ser Pro Ser Leu Lys Ser Thr Ala Asp Glu Lys Arg Val Ala  
169 405 410 415  
171 Ser Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu His Pro Thr Lys Glu  
172 420 425 430  
174 Ile Lys Ser Arg Gly Pro Glu Thr Ala Glu Leu Thr Arg Ser Phe Pro  
175 435 440 445  
177 Ser Glu Lys Arg Gly Val Leu Ser Ser Tyr Pro Ser Asp Val Ile Ser  
178 450 455 460  
180 Tyr Arg Gly Leu Arg Gly Ser Gln Asp Lys Leu Val Ser Pro Thr Asp  
181 465 470 475 480  
183 Ser Pro Gly Asp Cys Met Asp Arg Glu Lys Ile Glu Lys Asp Ser Gly  
184 485 490 495  
186 Leu Ser Ser Thr Ser Ala Gly Ser Glu Glu Phe Ser Thr Pro Glu  
187 500 505 510  
189 Val Ala Ser Ser Phe Ser Ser Asp Tyr Asn Val Ser Ser Leu Glu Asp  
190 515 520 525  
192 Arg Pro Ser Gln Glu Thr Ile Asn Cys Gly Asp Leu Asp Cys Arg Pro  
193 530 535 540  
195 Pro Gly Thr Gly Gln Ser Leu Lys Pro Glu Asp His Gly Tyr Gln Cys  
196 545 550 555 560  
198 Lys Ala Leu Pro Leu Ala Arg Leu Ser Pro Thr Asn Ala Lys Arg Phe  
199 565 570 575  
201 Lys Thr Glu Glu Arg Pro Ser Asn Val Asn Ile Ser Gln Arg Leu Pro  
202 580 585 590  
204 Gly Pro Gln Ser Thr Ser Ala Ala Glu Val Asp Val Ala Ile Lys Met  
205 595 600 605  
207 Asn Lys Arg Ile Val Leu Leu Glu Phe Ser Leu Ser Ser Leu Ala Lys  
208 610 615 620  
210 Arg Met Lys Gln Leu Gln His Leu Lys Ala Gln Asn Lys His Glu Leu  
211 625 630 635 640  
213 Ser Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala

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214	645	650	655
216	Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Ser Met Phe Ala Glu		
217	660	665	670
219	Met Glu Ile Leu Gly Gln Phe Asn Leu Gly Phe Ile Val Thr Lys Leu		
220	675	680	685
222	Lys Glu Asp Leu Phe Leu Val Asp Gln His Ala Ala Asp Glu Lys Tyr		
223	690	695	700
225	Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Ala Gln Arg Leu		
226	705	710	715
228	Ile Thr Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu Ala Val Leu		
229	725	730	735
231	Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp Phe Val Ile		
232	740	745	750
234	Asp Glu Asp Ala Pro Val Thr Glu Arg Ala Lys Leu Ile Ser Leu Pro		
235	755	760	765
237	Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Ile Asp Glu Leu Ile		
238	770	775	780
240	Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro Ser Arg Val		
241	785	790	795
243	Arg Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val Met Ile Gly		
244	805	810	815
246	Thr Ala Leu Asn Ala Ser Glu Met Lys Lys Leu Ile Thr His Met Gly		
247	820	825	830
249	Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro Thr Met Arg		
250	835	840	845
252	His Val Ala Asn Leu Asp Val Ile Ser Gln Asn		
253	850	855	
256	<210> SEQ ID NO: 6		
257	<211> LENGTH: 3056		
258	<212> TYPE: DNA		
259	<213> ORGANISM: Mus musculus		
261	<400> SEQUENCE: 6		
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264	gtctttccc gagagcggca ccgcaactct cccgcgggtga ctgtgactgg aggagtccctg 180		
265	catccatggaa gcaaaccgaa ggcgtgagta cagaatgtgc taaggccatc aagcctattg 240		
266	atgggaagtc agtccatcaa atttggcttg ggcaggttat actcagttt agcaccgtg 300		
267	tqaaggaggat gatagaaaaat agttagatg ctgggtctac tactattgt ctaaggctta 360		
268	aagactatgg ggtggacctc attgaaggat cagacaatgg atgtgggta gaagaagaaa 420		
269	actttgaagg tctagctctg aaacatcaca catctaagat tcaagaggat gccgaccta 480		
270	cgcaggttga aacttccggc ttccgggggg aagctctgat ctctctgtgt gcactaagtg 540		
271	atgtcaat atctacatgc cacgggtctg caagcgttgg gactcgactg gtgtttgacc 600		
272	ataatggaa aatcaccccg aaaactccct accccccgacc taaaggaacc acagtca 660		
273	tgcagcactt attttataca ctacccgtgc gttacaaaaga gtttcagagg aacattaaaa 720		
274	aggagtattt caaaatggtg caggtcttac aggctactg tatcatctca gcaggcgtcc 780		
275	gtgttaagctg cactaatcag ctcggacagg ggaagcggca cgctgtgtg tgacacaagcg 840		
276	gcacgtctgg catgaaggaa aatatcggt ctgtgtttgg ccagaagcag ttgcaaaagcc 900		
277	tcatttcctt tgttcagctg cccccctagtg acgctgtgtg tgaagagatc ggctgagca 960		
278	cttcaggacg ccacaaaacc ttttctacgt ttccggcttc atttcacagt gcacgcacgg 1020		

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279 cgccggagg agtgcacac acaggcagg tttcttcate aatcagaggc cctgtgaccc 1080  
 280 agcaaaggc tcataagctt tcaatgagg tttatcacat gtataaccgg catcagtacc 1140  
 281 catttgtcgt ccttaacgtt tccgttact cagaatgtgt ggatattaat gtaactccag 1200  
 282 ataaaaggca aattctacta caagaagaga agctattgtc ggcgtttt aagacctcct 1260  
 283 ttagatggaaat gtttgcacgt gatgcacaca agcttaatgt caaccagcag ccactgctag 1320  
 284 atgttgaagg taacttagt aagctgcata ctgcagaact agaaaaggct gtgccaggaa 1380  
 285 agcaagataa ctctccttca ctgaagagca cagcagacga gaaaaggta gcattccatct 1440  
 286 ccaggcttag agaggcctt tctttcatc ctactaaaga gatcaagtct aggggtccag 1500  
 287 agactgctga actgacacgg agtttccaa gtgagaaaag gggcgtgtt tcctttatc 1560  
 288 cticagacgt catctttac agggcctcc gtggctcgca ggacaaattt gtgagtccc 1620  
 289 cggacagccc tggactgt atggacagag agaaaataga aaaagactca gggctcagca 1680  
 290 gcacctcage tggctctgag gaagagttca gcaccccaaga agtggccagt agcttagca 1740  
 291 gtgactataa cgttagctcc ctagaagaca gaccttctca gggaaaccata aactgtggt 1800  
 292 acctggactg ccttccttca ggtacaggac agtcttgc ggcagaagac catggatatc 1860  
 293 aatgcacaaac tctacctcta gctcgtctgt caccacaaaa tgccaagcgc ttcaagacag 1920  
 294 aggaaaagacc ctcaaatgtc aacatttctc aaagattgcc tggctctcag agcacctcag 1980  
 295 cagctgaggt cgtatgtacc ataaaaatgt aatagagaat cgtgctcctc gagttctctc 2040  
 296 ttagttcttct agctaagcga atgaagcgt tacagcacct aaaggcgcag aacaaacatg 2100  
 297 aactgaggtt cagaaaattt agggccaaga tttggccctgg agaaaaccaa gcagcagaag 2160  
 298 atgaactcag aaaagagatt agtaaatcga tggatgcaga gatggagatc ttgggtcagt 2220  
 299 ttaacctggg atttatgtt accaaactga aagaggacct cttcctggt gaccagcatg 2280  
 300 ctgcggatga gaagtacaac tttgagatgc tgcagcagca cacgggtgc caggcgcaga 2340  
 301 ggctcatcac accccagact ctgaacttta ctgcgtcata tgaagctgtt ctgatagaaa 2400  
 302 atctggaaat attcagaaag aatggctttt actttgtcat ttagtggatgatc gctccagtca 2460  
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 305 gagtcagaca gatgtttgct tccagagcc tgcggaaatc agtggatgatt ggaacggcgc 2640  
 306 tcaatgcgag cgagatgaag aagctcatca cccacatggg tgagatggac caccctgg 2700  
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 308 actgacacac cccttgttagc atagagttt ttacagattt ttcgggttgc aaagagaagg 2820  
 309 ttttaagtaa tctgatttac gttgtacaaa aattagcatg ctgtttaat gtactggatc 2880  
 310 catttaaaag cagtgttaag gcaggcatga tggagtgtt cttctagctca gctacttggg 2940  
 311 tgatccggtg ggagctcatg tgagccagg actttgagac cactccgagc cacattcatg 3000  
 312 agactcaatt caaggacaaa aaaaaaaaaa tattttgaa gccttttaaa aaaaaaa 3056

315 &lt;210&gt; SEQ ID NO: 7

316 &lt;211&gt; LENGTH: 862

317 &lt;212&gt; TYPE: PRT

318 &lt;213&gt; ORGANISM: Homo sapiens

320 &lt;400&gt; SEQUENCE: 7

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324	Pro	Ile	Asp	Arg	Lys	Ser	Val	His	Gln	Ile	Cys	Ser	Gly	Gln	Val
325					20			25				30			
327	Leu	Ser	Leu	Ser	Thr	Ala	Val	Lys	Glu	Leu	Val	Glu	Asn	Ser	Leu
328					35			40				45			
330	Ala	Gly	Ala	Thr	Asn	Ile	Asp	Leu	Lys	Leu	Lys	Asp	Tyr	Gly	Val
331					50			55				60			
333	Leu	Ile	Glu	Val	Ser	Asp	Asn	Gly	Cys	Gly	Val	Glu	Glu	Asn	Phe
334					65			70				75			80

**VERIFICATION SUMMARY**

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L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:84 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4